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MITOGENOME ANNOUNCEMENT

Complete mitogenomic sequence of the Critically Endangered Northern River Shark *Glyphis garricki* (Carcharhiniformes: Carcharhinidae)

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Abstract

In this study we describe the first complete mitochondrial sequence for the Critically Endangered Northern River shark *Glyphis garricki*. The complete mitochondrial sequence is 16,702 bp in length, contains 37 genes and one control region with the typical gene order and transcriptional direction of vertebrate mitogenomes. The overall base composition is 31.5% A, 26.3% C, 12.9% G and 29.3% T. The length of 22 tRNA genes ranged from 68 (tRNA-*Ser2* and tRNA-*Cys*) to 75 (tRNA-*Leu1*) bp. The control region of *G. garricki* was 1067 bp in length with high A + T (67.9%) and poor G (12.6%) content. The mitogenomic characters (base composition, codon usage and gene length) of *G. garricki* were very similar to *Glyphis glyphis*.

Keywords

Glyphis garricki, mitochondrial genome, threatened species

History

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The euryhaline Northern River shark *Glyphis garricki* is listed as Critically Endangered in the IUCN Red List of Threatened Species (Pogonoski & Pollard, 2003) and Endangered in the Australian *Environment Protection and Biodiversity Conservation Act*. This poorly-known species of river shark (*Glyphis*: Carcharhinidae) was only recently formally described (Compagno et al., 2008); previous taxonomic uncertainty, rarity and a restricted distribution in remote estuaries and tidal rivers of northern Australia and southern New Guinea (Pillans et al., 2010) have limited available knowledge on the species. Here we provide the whole mitogenome of *G. garricki* and compare it with the recently published mitogenome of the Speartooth Shark *G. glyphis* (Chen et al., 2013b).

A tissue sample (fin clip) was collected from a specimen of *G. garricki* captured and released in the South Alligator River, Kakadu National Park, Northern Territory, Australia, under Kadadu Research Permit RK805. The experimental protocol and data analysis methods were according to Chen et al. (2013a). The complete mitochondrial sequence of *G. garricki* is 16,702 bp in length, contains 13 protein-coding genes, 2 rRNA genes, 22 transfer RNA genes and one control region (CR) (GenBank accession No. KF646786). The gene order and transcriptional direction are the same as those of typical vertebrate mitogenomes (Figure 1). The overall base composition is 31.5% A, 26.3% C, 12.9% G and 29.3% T, very similar to that of *G. glyphis* (31.5% A; 26.0% C; 13.0% G and 29.5% T) (Chen et al., 2013b). The usage of the start and stop codons of protein-coding genes in *G. garricki* is almost identical to *G. glyphis*, except the *ND6* gene which terminated by the AGA codon in *G. garricki* instead of the incomplete T as the stop codon in *G. glyphis* (Chen et al., 2013b).

The length of 22 tRNA genes ranged from 68 (tRNA-*Ser2* and tRNA-*Cys*) to 75 (tRNA-*Leu1*) bp and formed three conserved tRNA clusters (IQM, WANCY and HSL). All tRNAs could be folded into a cloverleaf second structure except for tRNA-*Ser2*, which lost the dihydrouridine arm and formed a simple loop. The origin of light-strand replication (OL) sequence (35 bp) was identified between tRNA-*Asn* and tRNA-*Cys* genes within cluster WANCY, which could initiate the replication of the light-strand by its hairpin structure. The CR of *G. garricki* is 1067 bp in length with high A + T (67.9%) and poor G (12.6%) content. In the CR, the three conserved sequence blocks (CSB1-3) were identified near the tRNA-*Phe* gene. In addition, these elements of *G. garricki* are completely identical to that of *G. glyphis*. The sequence identity of each gene compared with *G. glyphis* ranged from 93.93% (*ND5*) to 100.00% (tRNA-*Leu1*). Partial sequencing of *COI* (602 bp) and *CR* (421 bp) by Wynen et al. (2009) on *G. glyphis* and *G. garricki* reported 100.00% intraspecific similarity but 98.50% and 97.15% interspecific similarities for *COI* and *CR*, respectively, demonstrating they were distinct species. Whole gene sequencing in our study confirmed those results, although *COI* unexpectedly displayed lower similarity (97.62%) than the *CR* (97.66%).

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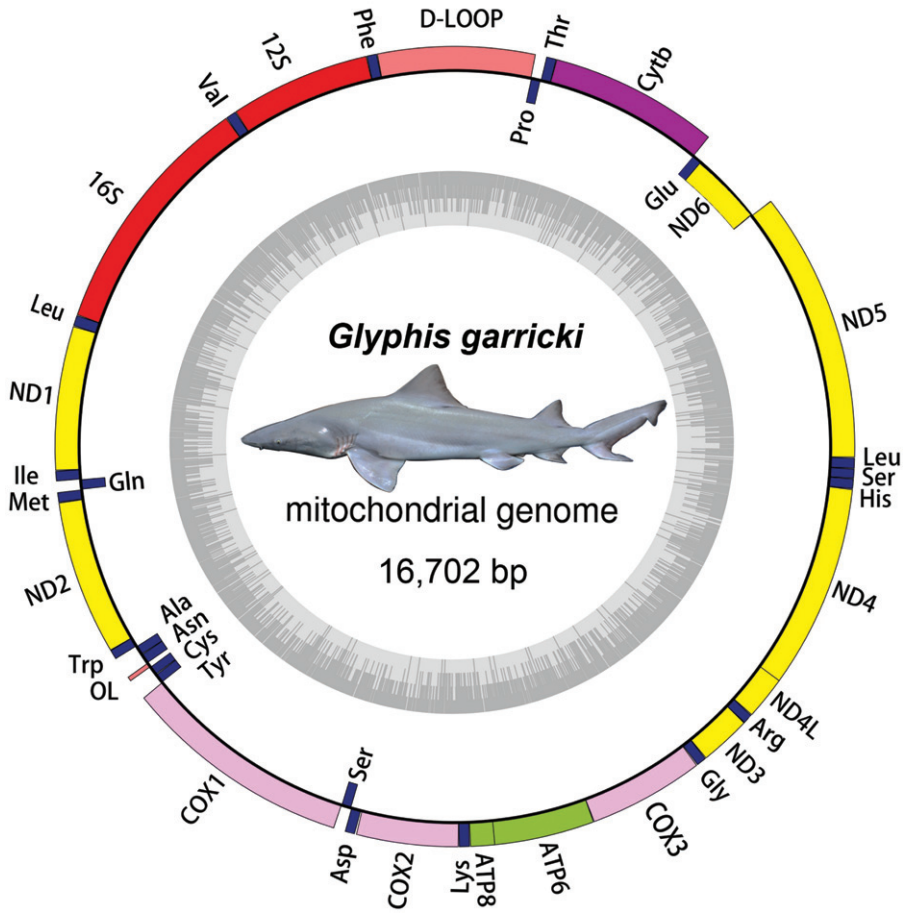
Figure 1. Mitogenomic map of *G. garricki*.



Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This study was supported by the Marine Biodiversity Hub, a collaborative partnership supported through funding from the Australian Government's National Environmental Research Program (NERP). Researcher PF was partly supported by the North Australia Marine Research Alliance (NAMRA). Researcher PMK was partly supported by the NERP Northern Australia Hub.

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